RE: pathogen TMDL document
Miller, Robin
to:
Rosella OConnor, Felix Locicero
03/08/2012 07:37 AM
Hide Details
From: "Miller, Robin" <Robin.Miller@hdrinc.com>

To: Rosella OConnor/R2/USEPA/US@EPA, Felix Locicero/R2/USEPA/US@EPA

Felix, Rosella:

The toughest comment to respond to is tabulating the loadings to the Hackensack and Passaic Rivers from Newark Bay as part of the LA.

There are 3 ways to do it:

1.   Way 1 – Run the model with loads coming directly into the Hackensack and Passaic Rivers set to 0 Enterococci concentration.  Add in code that will track the mass of Enterococci moving across the interface at the confluence of the Hackensack and Newark Bay and the confluence of the Passaic River and Newark Bay.  The code will determine the net mass after tracking the mass moving in both directions.  We have this code from other projects, but as far as I know, it is not in the pathogen model.  We've done this for Mark Tedesco to calculate the exchange of nitrogen in SWEM between the lower East River and Upper NY Bay, for example.

2.   Way 2 – Make a bounding approximation using the "tidal prism" volume flux at the mouth of the Hackensack and Passaic Rivers using an Enterococci concentration of 35/100 ml.  This ends up being a gross number rather than a net number and serves as an upper limit approximation.  I don't like this sort of approximation because it inflates the influence.

3.   Way 3 – Don't tabulate the load as one number and use a footnote to point to all the loads from the rest of the Harbor that drive what gets delivered to the Hackensack and Passaic via Newark Bay.

Right now, we have Way 3 in place and I'll develop some better explanation and include it in the WLA/LA summary chart that you suggested.  This is our "fail safe" for the 15$^{th}$.

In the meantime, we will work on Way 1.  I'm just concerned about getting it done by the 15$^{th}$.  By the 15$^{th}$ is doable, just tight and very assuming no problems.  We wouldn't have to run all 13 years, just 2000 and 2003 which control the TMDL condition.  Also, since we aren't trying to target different loading reduction percentages, there wouldn't be iterations, just running once for the two years.   I'll keep you posted as this progresses.

Robin

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**From:** Rosella OConnor [mailto:OConnor.Rosella@epamail.epa.gov]
**Sent:** Wednesday, March 07, 2012 3:20 PM
**To:** Miller, Robin
**Cc:** Felix Locicero
**Subject:** Re: pathogen TMDL document

Hi Robin,
Felix and I have looked through the document and marked it up with our comments. Overall the document looks good. One concern is the Margin of Safety. As you will see from the comments, we are concerned that the some of the implicit MOS factors are not really safety factors. Perhaps it's a matter of providing more information.

If you would like to discuss the comments, feel free to give us a call. I will be out tomorrow, but Felix will be in (vice-versa for Friday).
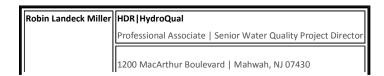
Thanks,
Rosella

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| From: | "Miller, Robin" <Robin.Miller@hdrinc.com> |
| To: | Rosella OConnor/R2/USEPA/US@EPA, Felix Locicero/R2/USEPA/US@EPA |
| Date: | 03/02/2012 01:15 PM |
| Subject: | pathogen TMDL document |

Felix and Rosella:

As we discussed, attached please find a draft of the pathogen TMDL document. Please let me know as soon as possible prior to March 15 if there is any EPA feedback or comments.

Robin

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[attachment "PCPathTMDLhackpass 3-1-12.doc" deleted by Rosella OConnor/R2/USEPA/US]